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                    GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on:       June  1, 2003, 16:20:34 ; Search time 247.669 Seconds
                                (without alignments)
                                10774.128 Million cell updates/sec

Title:        US-09-625-573-3
Perfect score: 1979
Sequence:     1 CAGGACTGCCTGAGACAAGC.........ATATGCAATATAAAATTTAG 1979

Scoring table: IDENTITY_NUC
              Gapop 10.0 , Gapext 1.0

Searched:     845702 seqs, 674182571 residues

Total number of hits satisfying chosen parameters:      1691404

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    Published_Applications_NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1943.8	98.2	143068	10	US-09-967-768A-316	Sequence 316, App
2	1081.4	54.6	1083	10	US-09-131-827A-1	Sequence 1, Appl
3	1079.8	54.6	1083	10	US-09-131-827A-19	Sequence 19, Appl
4	704.6	35.6	1059	12	US-10-106-623-19	Sequence 19, Appl
5	703.4	35.5	1225	10	US-09-813-653-14	Sequence 14, Appl
6	703.4	35.5	1376	9	US-10-086-814-2	Sequence 2, Appli
7	703.4	35.5	1376	10	US-09-796-202-2	Sequence 2, Appli
8	703.4	35.5	1477	10	US-09-759-841-1	Sequence 1, Appli
9	703.4	35.5	1477	10	US-09-938-719-2	Sequence 2, Appli
10	703.4	35.5	1477	10	US-09-939-226-2	Sequence 2, Appli
11	703.4	35.5	1477	10	US-09-938-703-2	Sequence 2, Appli
12	703.4	35.5	3383	10	US-09-734-221A-13	Sequence 13, Appl
13	703.4	35.5	3383	12	US-10-106-623-1	Sequence 1, Appli
14	703.4	35.5	1225	10	US-09-813-653-16	Sequence 16, Appl
15	701.8	35.5	1414	9	US-10-232-686-1	Sequence 1, Appl
16	701.8	35.5	1414	10	US-09-725-285-1	Sequence 1, Appli
17	701.8	35.5	1414	10	US-09-195-662A-1	Sequence 1, Appli
18	701.8	35.5	1414	10	US-09-339-912A-1	Sequence 1, Appli
19	701.8	35.5	1414	10	US-09-502-783A-1	Sequence 1, Appli

20	700.2	35.4	1414	10	US-09-779-879A-1	Sequence 1, Appli
21	700.2	35.4	1414	10	US-09-779-880A-1	Sequence 1, Appli
22	697.6	35.3	1056	10	US-09-779-879A-21	Sequence 21, Appl
23	697.6	35.3	1056	10	US-09-779-880A-21	Sequence 21, Appl
24	683.4	34.5	1442	10	US-09-938-719-3	Sequence 3, Appli
25	683.4	34.5	1442	10	US-09-939-226-3	Sequence 3, Appli
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27	376	19.0	792	10	US-09-938-719-1	Sequence 1, Appli
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30	350.2	17.7	1689	10	US-09-931-381A-15	Sequence 15, Appl
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33	348.8	17.6	1065	9	US-10-001-835-29	Sequence 29, Appl
34	341	17.2	3426	9	US-10-120-394-19	Sequence 19, Appl
35	304	15.4	1607	9	US-09-764-413-19	Sequence 19, Appl
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38	277.2	14.0	1318	10	US-09-789-482-3	Sequence 3, Appli
39	268.4	13.6	1487	10	US-09-789-486-3	Sequence 3, Appli
40	268.4	13.6	1487	10	US-09-954-456-267	Sequence 267, App
41	266.8	13.5	3100	10	US-09-954-456-945	Sequence 945, App
42	266.8	13.5	3100	10	US-09-954-456-1588	Sequence 1588, Ap
43	266.8	13.5	3100	10	US-09-104-792-1	Sequence 1, Appli
44	261.2	13.2	1586	10	US-09-912-025-1	Sequence 1, Appli
45	181.6	9.2	1050	10		

ALIGNMENTS

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RESULT 1
US-09-967-768A-316
; Sequence 316, Application US/0996776768A
; Patent No. US2002015087741
; GENERAL INFORMATION:
;  APPLICANT: Augustus, Meena
;  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sig
;  TITLE OF INVENTION: Sets
;  FILE REFERENCE: 689290-72
;  CURRENT APPLICATION NUMBER: US/09/967,768A
;  CURRENT FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: US/60/236,109
;  PRIOR FILING DATE: 2000-09-28
;  PRIOR APPLICATION NUMBER: US/60/236,034
;  PRIOR FILING DATE: 2000-09-28
;  PRIOR APPLICATION NUMBER: US/60/236,111
;  PRIOR FILING DATE: 2000-09-28
;  NUMBER OF SEQ ID NOS: 325
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 316
;  LENGTH: 143068
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-09-967-768A-316

  Query Match             98.2%;  Score 1943.8;  DB 10;  Length 143068;
  Best Local Similarity   99.9%;  Pred. NO. 0;
  Matches 1945;  Mismatches   0;  Conservative   0;  Indels   0;  Gaps   0;

Qy      27 CTGAACAGAGAAAGTGGATTGAACAAGGACGACGCATTCCCAGTACATCCACAACATGCTG 86
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Db   46052 CAGAACAGAGAAAGTGGATTGAACAAGGACGACGCATTCCCAGTACATCCACAACATGCTG 46111

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Qy   267 GTCGTCCTCATCTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTC 326
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Qy   327 AACCTGGCCATCCTGATCCTGCTTTTCTTATTACTCTCCCATTGTGGCTCACTCTGCT 386
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Qy   447 GGTTATTTTGGCCGGAATCTTCTCATCATCCTCCTGACAATCGATAGATACCTGGCTATT 506
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Qy  1827 CACCTTACATTGAAATCTATGAAATATCATGTCCATTGTGTGTCAGATGCTTCTTAGGCCA 1886
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Qy  1947 TGCTAATATATGTATATGCAATATAA 1973
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Best Local Similarity  99.9%;  Pred. No. 0;
Matches 1082;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

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Qy   141 ACCACCTTTTTGATTATGATTACGGTGCTCCCGTGCTCATAAATTGACGTGAAGCAAATT 200
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Qy   561 AGTGTGATCACCTGGTTGGTGCTGTTGCTTGCTTCTCGTGTTCCCAGGAATCATCTTTACTAAA 620
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Qy   621 TGCCAGAAAGAAGATTCTGTTATGTCGTGTGGCCCTTATTTCTCCACGAGGATGAATAAT 680
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Qy   681 TTCCACACAATAATGAGGAACACATTTGGGCGGTCCTCGCGCTCTCATCGGTCATC 740
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Db   601 TTCCACACAATAATGAGGAACACATTTGGGCGGTCCTCGCGCTCTCATCGGTCATC 660

Qy   741 TGCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAGGCATAGG 800
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Qy   801 GCAGTGAGTCATCTCACCATCATGATGTTACTTCTCTCTGGACTCCCTATAAC 860
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Qy   921 AGTCAACTGACCAAGCCACCAGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATC 980
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Qy   981 AATCCCATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTCTTC 1040
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Qy  1041 CGAAAGCACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTG 1100
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Qy  1101 GATGGAGTGACTTCAACAAACACGCCTTCCACTGGGCAGCAGGAGTCTCGGCTGGTTTA 1160
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Db  1021 GATGGAGTGACTTCAACAAACACGCCTTCCACTGGGCAGCAGGAGTCTCGGCTGGTTTA 1080

Qy  1161 TAA 1163
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Db  1081 TAA 1083
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RESULT 3
US-09-131-827A-19
; Sequence 19, Application US/09131827A
; Patent No. US2002003846A1
; GENERAL INFORMATION:
;   APPLICANT: Dean, Michael
;   APPLICANT: O'Brien, Stephen J.
;   APPLICANT: Smith, Michael
;   APPLICANT: Carrington, Mary
;   TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
;   TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
;   FILE REFERENCE: 14014.0333
;   CURRENT APPLICATION NUMBER: US/09/131,827A
;   CURRENT FILING DATE: 1998-08-10
;   PRIOR APPLICATION NUMBER: 60/055,659
;   PRIOR FILING DATE: 1997-08-14
;   NUMBER OF SEQ ID NOS: 20
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 1083
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-131-827A-19

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Query Match            54.6%;  Score 1079.8;  DB 10;  Length 1083;
Best Local Similarity  99.8%;  Pred. No. 6.5e-315;
Matches 1081;  Conservative  0;  Mismatches  2;  Indels  2;  Gaps  0;

Qy    81 ATGCTGTCCAATCTCGTTCTCGGTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTC 140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGCTGTCCAATCTCGTTCTCGGTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTC  60

Qy   141 ACCACCTTTTTGATTATGATTACGGTGCTCCCGTGCTCATAAATTGACGTGAAGCAAATT 200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 ACCACCTTTTTGATTATGATTACGGTGCTCCCGTGCTCATAAATTGACGTGAAGCAAATT 120

Qy   201 GGGGCCCAACTCCTGCCTCACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAAC 260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGGGCCCAACTCCTGCCTCACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAAC 180

Qy   261 ATGCTGGTCGTCCTCCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTAC 320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATGCTGGTCGTCCTCCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTAC 240

Qy   321 CTGCTCAACCTGGCCATCTCGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCAC 380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CTGCTCAACCTGGCCATCTCGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCAC 300

Qy   381 TCTTGCTGCAAATGAGTGGTCGTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTAT 440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TCTTGCTGCAAATGAGTGGTCGTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTAT 360

Qy   441 CACATCGGTTATTTTGGGCGGAATCTTCTTCATCATCATCCTGACAATCGATAGATACCTG 500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CACATCGGTTATTTTGGGCGGAATCTTCTTCATCATCATCCTGACAATCGATAGATACCTG 420

Qy   501 GCTATTGTCCATGCTGTGTTGCTTAAAAGCCAGGACGGTCACCTTTGGGGTGTGACA 560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GCTATTGTCCATGCTGTGTTGCTTAAAAGCCAGGACGGTCACCTTTGGGGTGTGACA 480

Qy   561 AGTGTGATCACCTGGTTGGTGCTGTTGCTTGCTTCTCGTGTTCCCAGGAATCATCTTTACTAAA 620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AGTGTGATCACCTGGTTGGTGCTGTTGCTTGCTTCTCGTGTTCCCAGGAATCATCTTTACTAAA 540
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                                    REFERENCE/DOCKET NUMBER: 27866/33670
                          TELECOMMUNICATION INFORMATION:
                              TELEPHONE: 312-474-6300
                              TELEFAX: 312-474-0448
                  INFORMATION FOR SEQ ID NO: 19:
                      SEQUENCE CHARACTERISTICS:
                          LENGTH: 1059 base pairs
                          TYPE: nucleic acid
                          STRANDEDNESS: single
                          TOPOLOGY: linear
                      MOLECULE TYPE: cDNA
                      FEATURE:
                          NAME/KEY: CDS
                          LOCATION: 1..1056
                      SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-106-623-19

Query Match             35.6%;  Score 704.6;  DB 12;  Length 1059;
Best Local Similarity   81.4%;  Pred. No. 1.1e-201;
Matches  834;  Conservative    0;  Mismatches  179;  Indels   12;  Gaps    1;

Qy    151 TTGATTATGATTACGGTGCTCCCTGCTCATAAATTTGACGTGAAGCAAATTGGGCCCAAC 210
          | ||||| |    |  | | |||| || |||| | ||  ||| ||| ||   |||||||
Db     35 TCGATTATTATACATCGGAACCCTGCCAAAAAATCAATGTGAAACAAATCCAGCCCGCC   94

Qy    211 TCCTGCCTCCGCTCTACTCGGTGTTCATCTTTGGTTTGTGGGCAACATGCTGGTCG 270
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db     95 TCCTGCCTCCGCTCTACTCGGTGTTCATCTTTGGTTTGTGGGCAACATACTGGTCG 154

Qy    271 TCCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACACTACCTGCTCAACC 330
          |||||||||| ||||| |||||| | |||||||||||||| ||||| |||||||||
Db    155 TCCTCATCCTGATAAACTGCAAAAGCTGAAAAGCTGACATGACTACCTGCTCAACC 214

Qy    331 TGGCCATCTCGATCTGCTTTTCTTATTACTCTCCCATTGTGGCTCACTCTGCTGCAA 390
          |||||||||||||||||||||||| |||||| |||| |||||||||||||||||||||
Db    215 TGGCCATCTCGACCTGCTTTTCCTTCTTACTGTCCCCTTCTGGGCTCACTGCTGCTG 274

Qy    391 ATGAGTGGGTCTTTGGGGATGCAATGCAAATTATTCACAGGCCTGTATCACATCGGTT 450
          ||                | ||| | |   | ||||| ||| |||||| ||  | |||
Db    275 CCCAGTGGGACTTTGGAAATACAATGTCAACTCTTGACAGGGCTCTATTTTATAGGCT 334

Qy    451 ATTTTGGCGGAATCTTCTTCATCATCCTCCTGCGAAATCGATAGATACCTGGCTATTCTCC 510
          ||||  ||||||||||||||||||||||||| |||||||||||||||||| |||| |||||
Db    335 TCTTCTCGGAATCTTCTTCATCATCCTCCTGCGAAATCGATAGGTACCTGGCTATCGTCC 394

Qy    511 ATGCTGTGTTTGCTTAAAAGCCAGGACGGTCACCTTGGGTGGTGGTGACAAGTGTGATCA 570
          |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db    395 ATGCTGTGTTTGCTTAAAAGCCAGGACAGTCACCTTTGGGTGGTGGTGACAAGTGTGATCA 454

Qy    571 CCTGGTTGGTGGCTGTGTTTGCTTCGTCCCAGGAATCATCTTTACTAAATGCCAGAAAG 630
          | |||||||||||||||| |||||||| ||||||||||||||| |||  ||||||||||
Db    455 CTTGGGTGGTGGCTGTGTGTTGCCTCTCCCCAGGAATCATCTTTACCAGATCTCAGAGAG 514

Qy    631 AAGATTCATTACGTTTATGTCTGTGGCCCTTATTTCCA----------CGAGGATGGAATA 678
          |||  | |||   | |||| |||  | | |||||||||          |  ||||||| |
Db    515 AAGGTCTTCATTACACCTGCAGCTCCATTTTCCATACGTCAGTATCAATTCTGGAAGA 574

Qy    679 ATTCCACACAATAATGAGGAACATTTTGGGGCTGCTCCTGCCCTCGTCATCATGGTCA 738
          ||||| || || | || | |||||||| |||| |||||||| ||  |||||||||||||
Db    575 ATTTTCAGACATTAAGATGTCATCGTTGCATCGTGGGGCTGGTCCTGCTGTCATGGTCA 634

Qy    739 TCTGCTACTCGGAATCCGGAATCCTGAAAACCCTGCTTCGTCGTGTCGAAACGAGAAGGCATA 798
          |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db    635 TCTGCTACTCGGAATCCGGAATCCTGAAAACTCGCTTCGTCGTGTCGAAACGAGAAGAGGCACA 694

Qy    799 GGGCAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTTCCTTCCTTCGGACTCCCTATA 858
          |||| |||||    | ||||  | | |||| |||| | | ||  ||  | ||| ||||||||
Db    695 GGGCTGTGAGCGTTATCTTCCCATCATGATAGTTTATTTCTTTCGTTGTGGGCTTCCCTACA 754

Qy    859 ACATTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACGTGAAAGCA 918
          ||  ||| || | |||||||||||||||||||||||||||||| || |||  ||||| ||
Db    755 ACATTGTCCCTCTCCCCGAACACCTTCCAGGAATTCTTTGGGCCTGAATAATTGCAGTAGCT 814

Qy    621 TGCCAGAAAGAAGATTCTGTTGTATGTCTGTGGCCCTTATTTCCACCAGGATGGGAATAAT 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGCCAGAAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTCCACCAGGATGGGAATAAT 600

Qy    681 TTCCACACAATAATGAGGAACATTTTGGGGCTGGTCCTGGCTCATCATGGTCATC 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TTCCACACAATAATGAGGAACATTTTGGGGCTGGTCCTGCTCATCATGGTCATC 660

Qy    741 TGCTACTCGGAATCCTGAAAACCCTGCTTCGTCGTGTCGAAACGAGAGAGAGGCATAGG 800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TGCTACTCGGAATCCTGAAAACCCTGCTTCGGTCGTGTCGAAACGAGAGAGGCATAGG 720

Qy    801 GCAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTTCTTCTTCTCGGACTCCCTATAAC 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GCAGTGAGTCATCTTCACCATCATGATTGTTTACTTTCTTCTTCTCGGACTCCCTATAAT 780

Qy    861 ATTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACC 920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 ATTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACC 840

Qy    921 AGTCAACTGGACCAAGCCACGCCACGTCTTGGGATGACACTCACTGCTGCATC 980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 AGTCAACTGGACCAAGCCACGCCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATC 900

Qy    981 AATCCCATCATCTATGCCTTCGTGGGGAGAAGTTCAGAGGTATCTCTCGGTGTTCTTC 1040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 AATCCCATCATCTATGCCTTCGTGGGGAGAAGTTCAGAGGTATCTCTCGGTGTTCTTC 960

Qy   1041 CGAAAGCACATCACCAAGCGCTTCTGCAAACATGTCCAGTTTTCTACAGGGGAGACAGTG 1100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CGAAAGCACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGGAGACAGTG 1020

Qy   1101 GATGGAGTGACTTCAACAAACACGCCCTTCCACTGGGAGCAGGAAGTCTCGGCTGTTTA 1160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GATGGAGTGACTTCAACAAACACGCCCTTCCACTGGGAGCAGGAAGTCTCGGCTGTTTA 1080

Qy   1161 TAA 1163
          |||
Db   1081 TAA 1083
```

RESULT 4
US-10-106-623-19
; Sequence 19, Application US/10106623
; Patent No. US2002015088A1
; GENERAL INFORMATION:
;   APPLICANT: Gray, Patrick W.
;   Schweickart, Vicky L.
;   Raport, Carol J.
;   TITLE OF INVENTION: Chemokine Receptor Materials and Methods
;   NUMBER OF SEQUENCES: 20
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;   STREET: 6300 Sears Tower, 233 S. Wacker Drive
;   CITY: Chicago
;   STATE: Illinois
;   COUNTRY: USA
;   ZIP: 60606
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/106,623
;   FILING DATE: 26-Mar-2002
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/771,276
;   FILING DATE: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;   NAME: No. US2002015088Aland, Greta E.
;   REGISTRATION NUMBER: 35,302

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Db   304  AGTGGGACTTGGAAATACAATGTGTCAACTCTTGACAGGGCTCTATTTATAGGCTTCT  363
               ||||||||||||||||||||||  ||||||||||||||  |||||||||
Qy   454  TTGGCGGAATCTTCTTCATCATCCTCTGACAATCGATAGATGATACTGGCTATTGTCCATG  513
               |||||||||||||||||||||| | ||||||||||| ||| |||||||||||
Db   364  TCTCTGGAATCTTCTTCATCATCCTCTGACAATCGATAGGTACCTGGCTGTCGTCCATG  423

Qy   514  CTGTGTTGCTTAAAAGCCAGGACGGTCACCTTGGGGTGTGACAAGTGTGATCACCT  573
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   424  CTGTGTTGCTTAAAAGCCAGGACGGTCACCTTGGGGTGTGACAAGTGTGATCACTT  483

Qy   574  GGTTGGTGGCTGTGTTGCTTGCCGTGTTGCCGTCTCCCCAGGAATCATCTTACTAAATGCCAGAAAGAAG  633
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   484  GGGTGGTGGCTGTGTTGCTTGCCGTGTTGCCGTCTCCCCAGGAATCATCTTACCAGATCATCAAAAAGAAG  543

Qy   634  ATTCTGTTTATGTCTGTGGCCCTTATTTCCA-----------CGAGGATGGAATAATT  681
               | |||||||||||||||||||||||| ||||          | ||||||||||| |
Db   544  GTCTTCATTACACCTGCAGCTCTCATTTTCCATACAGTCAGTATCAATTCTGAAGAATT  603

Qy   682  TCCACACAATAATGAGGAACATTTTGGGGCTGGTCTGGTCTCCGCCTCCCTATAACA  741
               |||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db   604  TCCAGACATTAAAGATAGTACACTTCTTGGGCTGCTCGTGGGCTCCCTTCATGGTCATCT  663

Qy   742  GCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGG  801
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   664  GCTACTCGGGAATCCTAAAAACTCTGCTTCGGTGTCGAAATGAGAAGAAGAGGCACAGGG  723

Qy   802  CAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTCCTCTGCTGGACTCCCTATAACA  861
               | ||| ||||||||||||||||||||| |||||||||||||  |||||||||||||||
Db   724  CTGTGAGGCTGTATCTTCACCATCATGATTGTTTATTTTCTCTGTTGGGCTCCCTACAACA  783

Qy   862  TTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCA  921
               ||||||| ||||||||||||||||||||||||||||||||||| |||| ||||||||
Db   784  TTGTCCTTCTCCTGAACACCTTCCAGGAATTCTTGGGCCTGAATAATTGCAGTAGCTCTA  843

Qy   922  GTCAACTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCA  981
               | |||||||||||||||||||||||||||| ||| |||||||||| ||||||||||||
Db   844  ACAGGTTGGACCAAGCCAGCTATGCAGGTGAGAGACCTTGGGATTGACGCCACTGCTGCATCA  903

Qy   982  ATCCCATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTCC  1041
               | |||||||||||||  ||||||||||||||||||||||| |||| | |||||||| ||||||
Db   904  ACCCCATCATCTATGCCTTTGTCGGGGAGAAGTTCAGAAACTACCTCTTAGTCTTCTTCC  963

Qy  1042  GAAAGCACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGGACAGTG  1101
               |||||||||||| |||| ||||||||||||||| |||||| |||||||||||||||||
Db   964  AAAAGCACATTGCCAAAGCTGCCAAACGCTTCCATCTTCCAAATGCTGTTCTATTTTCCAGCAAGAGGCTCCCG  1023

Qy  1102  ATGGAGTGACTTCAACAAACACGCCTTCAACAAAACACGCCTTCCACTGGGGAGCAGAGAAGTCTCGGCTGGTTTAT  1161
               | |||| ||| |||||||||| ||||||||||| ||||||||||||||||||||||||||
Db  1024  AGCCAGCAAGCTCAGTTTACACCCGATCCACTGGGGAGCAGGAGAAATATCTGTGGGCTTGT  1083

Qy  1162  AAAACGAGGAGCAGTTTGATTGT  1184
               ||| |||||||||||||||
Db  1084  GACACGGACTCAAGTGGGCTGGT  1106
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RESULT 6
US-10-086-814-2
; Sequence 2, Application US/10086814
; Publication No. US20030092632A1
; GENERAL INFORMATION:
;   APPLICANT: Dragic, Tatjana
;   APPLICANT: Olson, William C.
;   TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
;   FILE REFERENCE: 61010-AB-1
;   CURRENT APPLICATION NUMBER: US/10/086,814
;   CURRENT FILING DATE: 2002-02-28
;   NUMBER OF SEQ ID NOS: 38
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 1376
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-086-814-2

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Qy   919  CCAGTCAACTGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCA  978
               ||||||| ||  |||||| |||||||||||||||||||||||  |||||||||
Db   815  CTAACAGGTTGACCAAGCCATGCAGGTGACAGAGACTCTTGGGATGACACACTGCTGCA  874

Qy   979  TCAATCCCATCATCTATCGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCCGGTGTTCT  1038
               |||| ||||||||||||| |||||||| || |||||||||||| |  || ||||
Db   875  TCAACCCCATCATCTATCGCCTTCGTTGTCGGGGAGAAGTTCAGAAACTACCTCTTAGTCTTCT  934

Qy  1039  TCCGAAAGCACATCACCCAAGCCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAG  1098
               ||| |||||||||  ||  ||| ||||| |||| |||||||||  |||||||||||||
Db   935  TCCAAAAGCACATTGCCAAACGCTTCGCAAATCGTGTCCAAATTTCCAGCAAGAGGCTC  994

Qy  1099  TGGATGGAGTGACTTCAACAAACACGACCCTTCAACCGGGGAGCAGGAAGTCTCGGCTGGTT  1158
               ||| |||||| ||||  |||| ||  | |||||||||||||||||||||||||| |||||
Db   995  CCGAGCAAGCAAGTTCAGTTTACACCCGATCCACTGGGGAGCAGGAGGAAATATCTGTGGGCT  1054

Qy  1159  TATAA  1163
               | |
Db  1055  TGTGA  1059
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RESULT 5
US-09-813-653-14
; Sequence 14, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
;   APPLICANT: Nestor, John
;   APPLICANT: Wilson, Carol
;   APPLICANT: See, Raymond
;   APPLICANT: Tan Hehir, Christina
;   TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
;   FILE REFERENCE: CNS-005
;   CURRENT APPLICATION NUMBER: US/09/813,653
;   CURRENT FILING DATE: 2001-03-20
;   PRIOR APPLICATION NUMBER: US 60/190,946
;   PRIOR FILING DATE: 2000-03-21
;   PRIOR APPLICATION NUMBER: US 60/190,996
;   PRIOR FILING DATE: 2000-03-21
;   PRIOR APPLICATION NUMBER: US 60/191,299
;   PRIOR FILING DATE: 2000-03-21
;   NUMBER OF SEQ ID NOS: 44
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
;   LENGTH: 1225
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (27)..(1085)
US-09-813-653-14

Query Match   35.5%;
Best Local Similarity   80.5%;
Matches   840; Conservative   0; Mismatches   191; Indels 12; Gaps   1;
Score 703.4; DB 10; Length 1225;
Pred. No. 2.8e-201;

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Qy   154  ATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCCCAACTCC  213
               || ||  |||||||||||||||||||||||||| | ||||||||||||||||||||
Db    64  ATTATTATACATCGGAGCCCTGCCAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCC  123

Qy   214  TGCCTCCGCTCACTCGCTGCTGGTGTCATCTTGGTTTGTTGGTTTGTCATCTTTTGGTCGTGTCC  273
               || ||||| ||||| ||||| |||||||||| ||||||||||||| ||| ||||||||
Db   124  TGCCTCCGCTCACTCACTGTGTTTCATCTTTGGTTTGTTGTGGGCAACATGTGGTCATCC  183

Qy   274  TCATCTTAATAAACTGCAAAAAGTCGAAGTGCTTGACATTACCTGCTCAACCTGG  333
               || || ||||||||||||||| | |||||||| ||| || |||||||||||||||
Db   184  TCATCCTGATAAACTGCAAAAGGCTGAAGAGCCATGACATGACTACCTGCTCAACCTGG  243

Qy   334  CCATCTCTGATCTGCTGTTTTCTTATTACTCTCCCATTGTGGCTGCTCACTCTGCTCAAATG  393
               ||||| | | |||||| || |||| |||||||||||||||||||||||||||||||||||
Db   244  CCATCTCTGACCTGTTTTTCCTTCTACTGTCCCCTTCTACTGGGCCTCACTATGCTCCCCCC  303

Qy   394  AGTGGGTCTTTGGAATGCAATGTGCAAATTATTCACCAGGCTTGTACATCACATCCGGTTATT  453
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Qy 1162 AAAACGAGGAGCAGTTGATTGT 1184
              ||| ||| | |||
Db 1297 GACACGGACTCAAGTGGCTGGT 1319

RESULT 7
US-09-796-202-2
; Sequence 2, Application US/09796202
; Patent No. US20020068813A1
; GENERAL INFORMATION:
;   APPLICANT: Dragic, Tatjana
;   APPLICANT: Olson, William
;   TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
;   FILE REFERENCE: 2048/61010/JPW/SHS
;   CURRENT APPLICATION NUMBER: US/09/796,202
;   CURRENT FILING DATE: 2001-02-28
;   NUMBER OF SEQ ID NOS: 17
;   SOFTWARE: PatentIn version 3.0
;   SEQ ID NO 2
;   LENGTH: 1376
;   TYPE: DNA
;   ORGANISM: human
US-09-796-202-2

Query Match   35.5%;   Score 703.4; DB 10; Length 1376;
Best Local Similarity 80.5%;   Pred. No. 3e-201;
Matches 840; Conservative   0; Mismatches 191; Indels 191; Gaps 1;

Qy 154 ATTATGATTACGGTGCTCCCTGTCATAAATTGACGTGAAGCAAATTGGGCCCAACTCC 213
Db 277 ATTATTATACATCGGAGCCCTGCCAAAAATCAATGTGAAGCAAATCGCAGCCCGCCCTCC 336

Qy 214 TGCCTCCGCTCTACTCGCTGGTGTTCATCTTGGTTTGTGGGCAACATGCTGGTCGTCC 273
Db 337 TGCCTCCGCTCTACTCACTGGTGTTCATCTTGGTTTGTGGGCAACATGCTGGTCATCC 396

Qy 274 TCATCTTAATAAACTGCAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTCAACCTGG 333
Db 397 TCATCCTGATAAAACTGCAAAAGGCTGAAGAGCATGCATGCCACTACCTGCTCAACCTGG 456

Qy 334 CCATCTCTGATCTGCTTTTTTCATTACCTCCCATTGTGGCCTCACTCTGCTGCAAATG 393
Db 457 CCATCTCTGACCTGTTTTTCCTTCTTACTGCTCCCTTCTGGGCTCACTATGCTGCCGCCC 516

Qy 394 AGTGGGTCTTTGGGAATGCAAATTATTCACAGGCTGTATCACATCGGTTATT 453
Db 517 AGTGGGACTTTGGAAATACAATGTCAACTCTTGCAACTCTTTATTTATAGGCTTCT 576

Qy 454 TTGGCGGAATCTTCTTCACATCCTCCTGACAATCGATAGATACCTGGCTATTGTCCATG 513
Db 577 TCTCTGGAATCTTCTTCATCATCCTCCTGACAATCGATAGGTAGCCTGGTCGTCGTCCATG 636

Qy 514 CTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGATCACCT 573
Db 637 CTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTAGCCTGGTCATCT 696

Qy 574 GGTTGGTGGCGTGTTTGCGTGTCCCCTTATTTCCA 633
Db 697 GGGTAGTGGCCGTGTTGCGTGTCTCCCCGGAATCATCTTTACCAGATCATCAAAAGAAG 756

Qy 634 ATTCTGTTTATGTCTGTGGCCCTTATTTCCA--------CGAGGATGGAATAATT 681
Db 757 GTCTTCATTACACCTGCGAGCTCATTTTCCATACAGTCAGTATCAATTCTGGAAGAATT 816

Qy 682 TCCACACAATAATGAGGAACATTTTCAGAAGTTCAGAAACCTATCTCTCGGTTGTTCTTCC 741
Db 817 TCCAGACATTAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCCGCTGTCATGGTCATCT 876

Qy 742 GCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGAGGCATAGGG 801
Db 877 GCTACTCGGGAATCCTAAAAACTCTGCTTCGGTGTCGAAATGAGAAGAAGAGGCTCCCG 936

Qy 802 CAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTTCCTCTTCTGACTCCCTATAACA 861
Db 937 CGTACTCGGGAATCGCTTCTAAAAGCCAAGAGCGTCACCTTGGCGTGTCATCGGGAATCATGATTGTTTACTTTCCTCTTCTCTTCGGGCTCCCTACAACA 996

Qy 862 TTGTCATTCCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCA 921
Db 997 TTGTCCTTCCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAATAATTGCAGTAGCTCTA 1056

Qy 922 GTCAACTGGACCAAGCCACGCACGGAGTCACAGTGGGATGACTCACTGCTGCATCA 981
Db 1057 ACAGGTTGGACCAAGCTATGCAGGTGACAGACTCTTGGGATGACGCCACTGCTGCATCA 1116

Qy 982 ATTCTGTTTATGTCTGTGGCCCTTATTTCCA---------CGAGGATGGAATAATT 1041
Db 1117 GTCTTCATTACACCTGCGAGCTCATTTTCCATACAGTCAGTATCAATTCTGGAAGAATT 1176

Qy 1042 GAAAGCACATCACCACCAGTTCTCTGCAAACAATGTCCAGTTTTCTACAGGAGACAGTGG 1101
Db 1177 AAAAGCACATTGCCAAACGCTTCTGCAAATGCTGTTCTATTTTCCACCAAGAGGCTCCCG 1236

Qy 1102 ATGGAGTGACTTCAACAAACCGCCTTCACCTGGGGAGCAGGAAGTCGGCTGGTTTAT 1161
Db 1237 AGCGAGCAAGCTCAGTTACACCCGATCCCACTGGGGAGCAGGAAATATCTGTGGGCTTGT 1296

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Db   334 CCATCTCTGATCTGCTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCGCAAATG 393
             |||||||| ||| |||| ||||||||| |||||  || |||||
Db   457 CCATCTCTGACCTGTTTTCCTTTCCTTACTGTCTCCCCTTCTGGGCTCACTATGCTGCCCCC 516

Qy   394 AGTGGGTCTTTGGAATGCAATGCAAATTATTCACCAGGCGTGATCACATCGGTTATT 453
         |||||||| |||||| |||||||||||| || |||||||||| || | ||||
Db   517 AGTGGGACTTTGGAAATACAATGTGTCAACTCTTGCACAGGGCTCTATTTTTAGGCTTCT 576

Qy   454 TTGGCGGAATCTTCATCATCCTGACAATCGATAGATACCTGGCTATTGTCCATG 513
         ||||||||||||||||||||||||||||||||||||||||||| | |||||||
Db   577 TCTCTGGAATCTTCTTCATCATCCTGACAATCGATAGGTACCTGGCTGTCGTCCATG 636

Qy   514 CTGTGTTGCTTAAAGCCAGGACGGTCACCTTTGGGTGTGACAAGTGTGATCACCT 573
         |||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   637 CTGTGTTGCTTTAAAGCCAGGACGGTCACCTTTGGGTGTGACAAGTGTGATCACTT 696

Qy   574 GGTGGTGGCTGTGTTTGCTGTCTGTCCAGGAATCATCTTACTAAATGCCAGAAAGAAG 633
         || ||||||||||||||||||||||  ||| |||||||||||||||||||||||||
Db   697 GGGTGGTGGCTGTGTTTGCGTCTCTCCAGGAATCATCTTTACCAGATCTCAAAAAGAAG 756

Qy   634 AATTCGTTTATCGTCTGGGCCCTTATTTCCA----------CGAGGATGGAATAATT 681
         ||  ||  ||| |||||||| ||||||||||          || ||||||||||||
Db   757 GTCTTCATTACACCTGCAGCTCTCATTTTCCATTACAGTCAGTATCAATTCTGGAAGAATT 816

Qy   682 TCCACACAATAATGAGGAACATTTTGGGGCTGGTCCGTCCTGCTCCGCTGCTCATGGTCATCT 741
          || || ||||||| |||||||| ||||||||||||||||||||||||||||||||||||||
Db   817 TCCAGACATTAAAGATAGTACATCTTGGGGGCTGGTCCTGCGGCTGGTTGTGCATGGTCATCT 876

Qy   742 GCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTGCAAACAGAGAAGAAGAGGCATAGGG 801
         |||||||||||||||||||||  |||||||||||||||||||||||||||||||||||||||| ||||
Db   877 GCTACTCGGGAATCCTAAAAACTCTGCTTCGGTGTGCAAATGAGAAGAAGAGGCACCAGGG 936

Qy   802 CACTGAGAGTCATCTTCACCATCATGATTGTTTACTTCTCTTGGACTCCCTATAACA 861
          | ||| ||  ||| ||||| |||||||||||||||| ||||||||||| ||||||||
Db   937 CTGTGAGGCTTATCTTCACCATCATGATGTTTATTTTCTCTCTGGGCTCCCCTACAACA 996

Qy   862 TTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGGCCTGAGTAACTGTGAAAGCACCA 921
         |||||||||||||||||||||||||||||||||||  || |||||||||||||||||||||
Db   997 TTGTCCTTCTCCTGAACACCTTCCAGGAATTCTTTGGGCCTGAATAATTGCAGTAGCTCTA 1056

Qy   922 GTCAACTGGACCAAGCCACGCAGCTGACAGAGACTCTTGGGATGACTCTGCATCA 981
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Db   1057 ACAGGTTGGACCAAGTATGCAGTGCAGTATGACGGACTCTGCATCA 1116

Qy   982 ATCCCATCATCATATGCCTTCGTTGGGGAGAAGTTCAGAGAAGGTATCTCTCCGGTGTTCTTCC 1041
         | |||||| |||||||||||| |||||||||| |||||||||||||||||| | |||||||||
Db   1117 ACCCCATCATCATATGCCTTTGTCGGGGGAGAAGTTCAGAAACTCAGAAACTACCTCTTTAGTCTTCTTCC 1176

Qy   1042 GAAAGCACATCACCAAGCCGCTTCTGCAAACAATGTCCAGTTTCTCACAGGGGAGACAGTGG 1101
         ||||| |||||||||||||||| ||||||||||||||||||||   |||||||||||||||||
Db   1177 AAAAGCACATTGCCAAAGCCTTCAAAATGCTGTTCTATTTCCAGCAGAAGTCTCCGCTGGTTAT 1236

Qy   1102 ATGGAGTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAGTCTCGGCTGGTTTAT 1161
         |||||||| ||| ||| |||||||||||||||||||||||||||||||||||||||||||
Db   1237 AGCCAGCAAGCTCAGTTTACACCCGATCCACCTGGGAGCAGGAGAAATATCTGTGGGCTTGT 1296

Qy   1162 AAAACGAGGAGCAGTTTGATTGT 1184
         | ||| |||||||||||||  |||
Db   1297 GACACGGACTCAAGTGGGGCTGGT 1319
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Db   937 CTGTGAGGCTTATCTTCACCATCATGATGTTTATTTTCTCTCTGGGCTCCCCTACAACA 996
             | |||||  | ||||||||||||||||||||||||||||||||||| |||||
Qy   862 TTGTCATTCTCCTGAACACCTTCCAGGAATTCTTTGGGCCTGAGTAACTGTGAAAGCACCA 921

Db   997 ACAGGTTGGACCAAGTATGCAGTGCAGTATGACGGACTCTGCATCA 1056
         ||||| ||||||||| |||||| |||||||||| |||||||||||||
Qy   922 GTCAACTGGACCAAGCCACGCAGCTGACAGAGACTCTTGGGATGACTCTGCATCA 981

Db   1057 ACAGGTTGGACCAAGTATGCAGTGCAGTATGACGGACTCTGCATCA 1116
          | ||||| |||||||||||| ||||| ||||||||||||||||||||
Qy   982 ATCCCATCATCATATGCCTTCGTTGGGGAGAAGTTCAGAGAAGGTATCTCTCCGGTGTTCTTCC 1041

Db   1117 ACCCCATCATCATATGCCTTTGTCGGGGGAGAAGTTCAGAAACTCAGAAACTACCTCTTTAGTCTTCTTCC 1176
          |||||| || ||||||||||| ||||||||||||||||||  ||||||||| ||||||||||||
Qy   1042 GAAAGCACATCACCAAGCCGCTTCTGCAAACAATGTCCAGTTTCTCACAGGGGAGACAGTGG 1101

Db   1177 AAAAGCACATTGCCAAAGCCTTCAAAATGCTGTTCTATTTCCAGCAGAAGTCTCCGCTGGTTAT 1236
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Qy   1102 ATGGAGTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAGTCTCGGCTGGTTTAT 1161

Db   1237 AGCCAGCAAGCTCAGTTTACACCCGATCCACCTGGGAGCAGGAGAAATATCTGTGGGCTTGT 1296
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Qy   1162 AAAACGAGGAGCAGTTTGATTGT 1184

Db   1297 GACACGGACTCAAGTGGGGCTGGT 1319
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RESULT 8
US-09-759-841-1
; Sequence 1, Application US/09759841
; Patent No. US2001003926A1
; GENERAL INFORMATION:
;   APPLICANT: Rickett, Graham A
;   APPLICANT: Dobbs, Susan
;   APPLICANT: Perros, Manoussos
;   TITLE OF INVENTION: Assay Method
;   FILE REFERENCE: PC10348APME
;   CURRENT APPLICATION NUMBER: US/09/759,841
;   CURRENT FILING DATE: 2001-01-12
;   PRIOR APPLICATION NUMBER: GB 0000661.9
;   PRIOR FILING DATE: 2000-01-12
;   PRIOR APPLICATION NUMBER: GB 0000663.5
;   PRIOR FILING DATE: 2000-01-12
;   PRIOR APPLICATION NUMBER: GB 0000659.3
;   PRIOR FILING DATE: 2000-01-12
;   NUMBER OF SEQ ID NOS: 6
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 1477
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1377, 1384, 1385
;   OTHER INFORMATION: n is a or g or c or t/u
US-09-759-841-1

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Query Match       35.5%;  Score 703.4;  DB 10;  Length 1477;
Best Local Similarity   80.5%;  Pred. No. 3.1e-201;
Matches  840;  Conservative  0;  Mismatches  191;  Indels  12;  Gaps  1;

Qy   154 ATTATGATTACGGTGCTCCCTGTCCCTGTCATAAATTGACGTGAAGCAAAATTGGGGCCCAACTCC 213
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Db   277 ATTATTATACAICGGAGCCCTGCCAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCC 336

Qy   214 TGCCTCCGCTCACTCCCTGGTGTTCATCTTGGTTTGTGGGCAACATGCTGGTCGTCC 273
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Db   337 TGCCTCCGCTCACTCACTGGTGTTCATCTTTGGTTTGTGGGCAACATGCTGGTCATCC 396

Qy   274 TCATCTTAATAAACTGCAAAAAGTCAAGTGCTTGACTGACATTTACCTGCTCAAACTGG 333
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Db   397 TCATCCTGATAAACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGG 456
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RESULT 9
US-09-938-719-2
; Sequence 2, Application US/09938719
; Patent No. US2002010674A1
; GENERAL INFORMATION:
;   APPLICANT: SAMSON, MICHEL
;   ,,   PARMENTIER, MARC
;   ,,   VASSART, GILBERT
;   ,,   LIBERT, FREDERICK
;   TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
;   ,,   AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

Qy   634 ATTCTGTTATGCTCGTGGCCCTTATTTCCA---------CGAGGATGGAATAATT   681
          | |||| ||| || || ||||||||
Db   757 GTCTTCATTACACCTGCAGCTCTCATTTCCATACAGTCAGTATCAATTCTGGAAGAATT   816

Qy   682 TCCACACAATAATGAGGAACATTTGGGCTGGTCCTCGCCGCTGCTCATCATGGTCATCT   741
          ||| || ||| || | |||||||||||||||||||||||||||||||||||
Db   817 TCCAGACATTAAAGATAGTCATCTTGGGCTGGTCCTCGCCGCTGCTCATCATGGTCATCT   876

Qy   742 GCTACTCGGGAATCCTGAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGG   801
          |||||||||||||||| |||| ||| |||||||||||||| |||||||||||||| ||||
Db   877 GCTACTCGGGAATCCTAAAAACCTCTGCTTCGGTGTCGAAATGAGAAGAAGAGGCACAGG   936

Qy   802 CAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACA   861
          | ||| | | ||||||||||||||||||||||| |||||||||||||| ||||| ||||
Db   937 CTGTGGAGGCTTATCTTCACCATCATGATTGTTTATTTTCTCTTCTGGGCTCCCTACAACA   996

Qy   862 TTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCA   921
          ||||| |||| ||||||||| |||||||||||| |||||||| || | || | |
Db   997 TTGTCCTTCTCTCTGAACACCCTTCCAGGAATTCTTTGGCCTGAATAATTGCAGTAGCTCTA   1056

Qy   922 GTCAACTGACCAAGCCACCGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCA   981
          |||||||| | |||| | |||||| | |||||||||||||||||| |||||||||||
Db 1057 ACAGTTGGACCAAGCTGACAGAGACTCTTGGGATGACGCCACTGCTGCATCA   1116

Qy   982 ATCCCATCATCTATGCTTCGTTGGGAGGAGTTCAGAAGGTATCTCGGTTGTTCTTCC   1041
          | ||| || || || ||| | ||||||||||| || | ||||||||||
Db 1117 ACCCCATCATCTATGCCTTTGTCGGGGAGAGTTCAGAGAGTTCAGAAAACTACCTCTTAGTCTTCTTCC   1176

Qy 1042 GAAAGCACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTCTCACAGGGAGACAGTGG   1101
          || || ||| || | | |||||||| ||||||| | | || ||||| |
Db 1177 AAAAGCACATTGCCAAACGCTTCTGCAAATGCTGTATTTCTATTTTCCAGCAAGAGGTCCCCG   1236

Qy 1102 ATGAGTGACTTCAACAAACACGCCTTCACCTGGGAGCAGGAAGTCTCGGCTGGTTTAT   1161
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Db 1237 AGCGAGCAAGCTCAGTTTTACACCCGATCCACTGGGGAGCAGGAGGAAATATCTGTGGGCTTGT   1296

Qy 1162 AAAACGAGGAGCAGTTGATTGT   1184
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Db 1297 GACACGGACTCAAGTGGGCTGGT   1319

RESULT 10
US-09-939-226-2
; Sequence 2, Application US/09939226
; Patent No. US20020110805A1
GENERAL INFORMATION:
    APPLICANT:
                SAMSON, MICHEL
                PARMENTIER, MARC
                VASSART, GILBERT
                LIBERT, FREDERICK
    TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
                        AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
    NUMBER OF SEQUENCES: 17
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: Knobbe, Martens, Olson & Bear
        STREET: 620 Newport Center Drive   16th Floor
        CITY: Newport Beach
        STATE: CA
        COUNTRY: U.S.A.
        ZIP: 92660
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/09/939,226
        FILING DATE: 24-Aug-2001
        CLASSIFICATION: <Unknown>
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: 09/626,939
        FILING DATE: 2000-07-27
    ATTORNEY/AGENT INFORMATION:

    NUMBER OF SEQUENCES: 17
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: Knobbe, Martens, Olson & Bear
        STREET: 620 Newport Center Drive   16th Floor
        CITY: Newport Beach
        STATE: CA
        COUNTRY: U.S.A.
        ZIP: 92660
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/09/938,719
        FILING DATE: 24-Aug-2001
        CLASSIFICATION: <Unknown>
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: 09/626,939
        FILING DATE: 27-JULY-2000
    ATTORNEY/AGENT INFORMATION:
        NAME: Altman, Daniel E
        REGISTRATION NUMBER: 34,115
        REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 1477 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: single
        TOPOLOGY: linear
    MOLECULE TYPE: DNA (genomic)
    FEATURE:
        NAME/KEY: CDS
        LOCATION: 240..1295
    SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-938-719-2

Query Match   35.5%; Score 703.4; DB 10; Length 1477;
Best Local Similarity   80.5%; Pred No. 3.1e-201;
Matches 840; Conservative   0; Mismatches 191; Indels   12; Gaps   1;

Qy   154 ATTATGATTACCGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCCCAACTCC   213
          ||||| || | ||||||||||| |||||||||||||||||| | | ||| ||||||
Db   277 ATTATTATACATCGGAGCCTGCACAAAAAATCAATGTGAAGCAAATCCGACCCGCCCTCC   336

Qy   214 TGCCTCCGCTCTCACTCCGCTGGTGTTCATCTTGTTCATCTTTGTTGTGGCAACATGCTGCTGTCGTCC   273
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Db   337 TGCCTCCGCTCTCACTCCGGTGGTGTTCATCTTTGTTCATCTTTGTTTGTGGCAACATGCTGTCATCC   396

Qy   274 TCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGAGTGCTTGACTGACATTTACCCTGCTCAACCTGG   333
          |||| | | ||||||||||||| |||||| | || ||| | |||||||||||| |||| |||||||||||||
Db   397 TCATCCTGATAAACTGCAAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGG   456

Qy   334 CCATCTCTGATCTGCTTTTTCTTTATTATACTCCTCCCATTGTGGGCTCACTCTGCTGCAAATG   393
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Db   457 CCATCTCTGACCTGTTTTTCTTTATTATTACTGTCCCCTTCGGGCTCACTATGCTGCCGCCC   516

Qy   394 AGTGGGTCTTTGGAATGCAAATGTGCAAATTATTCACCAGGCGTATCACATCGGTTATT   453
          |||||| ||||||||| ||||||| ||| | || ||||||| |||| | ||| | ||
Db   517 AGTGGGACTTTGGAAATACAATGTGTCAACTCTTGACAGGCGTCACCATTTGGGTGGTGATCACTT   576

Qy   454 TTGGCGGAATCTTCTTCATCATCCTCGACAATCGATAGATACCTGCTATTGTCCATG   513
          | ||||||||||||||||||||||| |||||||||||| |||||| |||||||||||
Db   577 TCTCTGGAATCTTCTTCATCATCCTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATG   636

Qy   514 CTGTGTTTGCTTAAAAGCCAGGACGGTCACCTTTGGGTGGTGTGACAAGTGTGATCACCT   573
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   637 CTGTGGTGGCTGTGTTTGCGTCTCTCCCAGGACGGTCACCTTTGGGTGGTGTGACAAGTGTGATCACTT   636

Qy   574 GGTTGGTGGCTGTGTTTGCTTCCTCGTCCCAGGAATCATCTTTACTAAATGCCAGAAAGAAG   633
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Db   697 GGGTGGTGGCTGTGTTTGCCGTCTCTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAG   756

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                 NAME: Altman, Daniel E
                 REGISTRATION NUMBER: 34,115
                 REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
     SEQUENCE CHARACTERISTICS:
          LENGTH: 1477 base pairs
          TYPE: nucleic acid
          STRANDEDNESS: single
          TOPOLOGY: linear
     MOLECULE TYPE: DNA (genomic)
     FEATURE:
          NAME/KEY: CDS
          LOCATION: 240..1295
     SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-939-226-2

Query Match             35.5%;  Score 703.4;  DB 10;  Length 1477;
Best Local Similarity   80.5%;  Pred. No. 3.1e-201;
Matches  840;  Conservative    0;  Mismatches  191;  Indels  12;  Gaps    1;

Qy   154 ATTATGATTACCGGTGCTCCCTGTCATAAATTGACGTGAAGCAAATTGGGCCCAACTCC 213
Db   277 ATTATTATACATCGGAGCCCTGCCAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCC 336

Qy   214 TGCCTCCGCTCACTCGCTGGTGTTCATCTTTGGTTTTGTGGCCAACATGCTGTCGTCC 273
Db   337 TGCCTCCGCTCTACTCACTGGGTGTTCATCTTTGGTTTTGTGGGCCAACATGCTGTCATCC 396

Qy   274 TCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTCAACCTGG 333
Db   397 TCATCCTGATAAACTGCAAAAGGCTGAAGAGCTGACATCTACCCTGCTCAACCTGG 456

Qy   334 CCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCAAATG 393
Db   457 CCATCTCTGACCTGTTTTTCCTTCTCTGTCCCCTTCTCCACTATGCTGCCGCCC 516

Qy   394 AGTTGGGTCTTGGGAATGCAAATGTGCAAATTATTCACACAGGCGTGTATCACATCGGTTATT 453
Db   517 AGTGGGACTTTGGAAATACAATCAATGTGTCAACTCTTATAGCAGGCGTCTCTATTTTATAGGCTTCT 576

Qy   454 TTGGCGGAATCTTCTTCATCATCCTCCTGACAATGCGATAGATACCTGGCTATTGTCCATG 513
Db   577 TCTCTGGAATCTTCTTCATCATCCTCCTGACAATGCGATAGGTACCTGGCGTCGTCCCATG 636

Qy   514 CTGTGTTTGCTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACCT 573
Db   637 CTGTGTTTGCTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTT 696

Qy   574 GGTTGGTGGCTGTGTTGCTTCTGTCTCCCAGGAAATCATCTTTACTAAATGCCAGAAAGAAG 633
Db   697 GGGTTGGTGGCTGTGTTGCTTCTGTCTCCCCAGGAATCATCATCTTTACCAGAATCTCAAAAAGAAG 756

Qy   634 ATTCTGTTTATGTCTGTGGCCCTTATTTCCA----------CGAGGATGGAATAATT 681
Db   757 GTCTTCATTACACCTGCAGCCTCTCATTTTTCCATACAGTCAGTATCAATTCTGGAGAATT 816

Qy   682 TCCACACAATAATGAGGAACATTTTGGGCGTCCTGGGTCCTGCGCGCTCATCATGGTCATCT 741
Db   817 TCCAGACATTAAAGATAGTCATCTTGGGGCGTCCTGGGTCCTGCGCGCTCATGGTCATCT 876

Qy   742 GCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTGTCGAAACGAGAAGAGGCATAGGG 801
Db   877 GCTACTCGGGAATCCTAAAAAACTCTGCTTCGGTGTCGAAATGAGAAGAAGAGGCACAGGG 936

Qy   802 CAGTGAGAGTCATCTTCACCATCATGATTGTTACTTTCTTCTTGGACTTCCCCATAACA 861
Db   937 CGTGAGGCCTTATCTTCACCATCATGATTGTTATTTTCTTCTTGGGCTCCCTCCTACAACA 996

Qy   862 TTGTCATTCTCGAACACCTTCCAGGAATTCTTCCGCCTCGAGTAACTGTGAAAGCACCA 921
Db   997 TTGTCCTTCCTCGAACACCTTCCAGGAATTCTTTGGCCTTGAATAATTGCAGTAGCCTCTA 1056

Qy   922 GTCAACTGGACCAAGCCACCGCAGGTGACAGAGACTCTTGGGATGACTCACTCTGCATCA 981
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Db  1057 ACAGGTTGGACCAAGCTATGCCTTCGTTGGGGAGGAGACTCTTGGGATGACGACCTGCTGCATCA 1116

Qy   982 ATCCCATCATCTATGCCTTCGTTGGGGAGGAGAGTTCAGAAGGTATCTCCGTGTTCTTCC 1041
Db  1117 ACCCCATCATCTATGCCTTCGTTGGGGAGGAGAGTTCAGAAACTACCTCTTAGTCTTCTCC 1176

Qy  1042 GAAAGCACATCACCAAGGCCTTCTGCAAACAATGTCCAGTTTTCTCACAGGGAGACAGTGG 1101
Db  1177 AAAAGCACATTGCCAAACGCTTCTGCAAATGCTGTCCAAAATGTCCATTTTCCAGCAAGAGGCTCCCG 1236

Qy  1102 ATGGAGTGACTTCAACAAACACCGCCTTCCACTGGGGAGCAGGAAGCTTCGGCGTGTTTAT 1161
Db  1237 AGGAGCAAGCTCAGTTTCACCCCATCCACTGGGGAGCAGGAAATATCTGTGGGCTTGT 1296

Qy  1162 AAAACGAGGAGCAGTTGATTGT 1184
Db  1297 GACACGGACTCAAGTGGGCTGGT 1319
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RESULT 11
US-09-938-703-2
; Sequence 2, Application US/09938703
; Patent No. US2002011870A1
; GENERAL INFORMATION:
     APPLICANT: SAMSON, MICHEL
                PARMENTIER, MARC
                VASSART, GILBERT
                LIBERT, FREDERICK
     TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
                AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
     NUMBER OF SEQUENCES: 17
     CORRESPONDENCE ADDRESS:
          ADDRESSEE: Knobbe, Martens, Olson & Bear
          STREET: 620 Newport Center Drive 16th Floor
          CITY: Newport Beach
          STATE: CA
          COUNTRY: U.S.A.
          ZIP: 92660
     COMPUTER READABLE FORM:
          MEDIUM TYPE: Floppy disk
          COMPUTER: IBM PC compatible
          OPERATING SYSTEM: PC-DOS/MS-DOS
          SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
     CURRENT APPLICATION DATA:
          APPLICATION NUMBER: US/09/938,703
          FILING DATE: 24-Aug-2001
          CLASSIFICATION: <Unknown>
     PRIOR APPLICATION DATA:
          APPLICATION NUMBER: 09/626,939
          FILING DATE: 2000-07-27
     ATTORNEY/AGENT INFORMATION:
          NAME: Altman, Daniel E
          REGISTRATION NUMBER: 34,115
          REFERENCE/DOCKET NUMBER: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
     SEQUENCE CHARACTERISTICS:
          LENGTH: 1477 base pairs
          TYPE: nucleic acid
          STRANDEDNESS: single
          TOPOLOGY: linear
     MOLECULE TYPE: DNA (genomic)
     FEATURE:
          NAME/KEY: CDS
          LOCATION: 240..1295
     SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-938-703-2

Query Match   35.5%; Score 703.4; DB 10; Length 1477;
Best Local Similarity   80.5%; Pred. No. 3.1e-201;
Matches 840; Conservative   0; Mismatches 191; Indels 12; Gaps   1;
US-09-938-703-2

Qy   154 ATTATGATTACCGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGCCCAACTCC 213

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US-09-734-221A-13
; Sequence 13, Application US/09734221A
; Publication No. US20030096221A1
; GENERAL INFORMATION:
;  APPLICANT: LITTMAN, DAN R.
;            DENG, HONGKUI
;            ELLMEIER, WILFRIED
;            LANDAU, NATHANIEL R.
;            LIU, RONG
;  TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
;                      MACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
;                      USES THEREOF
;  NUMBER OF SEQUENCES: 14
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: David A. Jackson, Esq.
;   STREET: 411 Hackensack Ave, Continental Plaza, 4th
;           Floor
;   CITY: Hackensack
;   STATE: New Jersey
;   COUNTRY: USA
;   ZIP: 07601
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/734,221A
;   FILING DATE: 11-Dec-2000
;   CLASSIFICATION: <Unknown>
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/666,020
;   FILING DATE: 19-JUN-1996
;   APPLICATION NUMBER: US 08/227,319
;   FILING DATE: 13-APR-1994
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Jackson Esq., David A.
;   REGISTRATION NUMBER: 26,742
;   REFERENCE/DOCKET NUMBER: 1049-1-004 N2
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 201-487-5800
;   TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 13:
;  SEQUENCE CHARACTERISTICS:
;   LENGTH: 3383 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;  MOLECULE TYPE: cDNA
;  HYPOTHETICAL: NO
;  ORIGINAL SOURCE:
;   ORGANISM: Homo sapiens
;  SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-734-221A-13

Query Match             35.5%;  Score 703.4;  DB 9;  Length 3383;
Best Local Similarity   80.5%;  Pred. No. 5.6e-201;
Matches  840;  Conservative  0;  Mismatches  191;  Indels  12;  Gaps  1;

Qy   154 ATTATGATTAGGGTGCTCCCTGTCATAAATTGACGTGAAGCAAATTGGGGCCCAACTCC 213
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Db    92 ATTATTATACATCGGAGCCCTGCCAAAAAATCAATGTGAAGCAAATCCGCAGCCCGCCTC 151

Qy   214 TGCCTCCGCTCACTCGCTGGTGTTCATCTTGTTTGTGGGCAACATGCTGGTCGTCC 273
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Db   152 TGCCTCCGCTCACTCACTGGTGTTCATCTTGTTTGTGGGCAACATGCTGGTCATCC 211

Qy   274 TCATCTTAATAAACTGCAAAAGCTGAAGTCGAAGTGCTTGACATTACCTGCTCAACCTGG 333
         |||| ||  ||  ||||||||||||||| |||||| |||||||||||||||||||||||
Db   212 TCATCCTGATAAACTGCAAAAGCTGAAAGGCTGAAGCATGACATCTACCTGCTCAACCTGG 271

Qy   334 CCATCTCTGATCTGCTTTTCTATTACTCTCCATTGTGGGCTCACTGTGCTGCAAATG 393
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Db   277 ATTATTATACATCGGAGCCGAGCCAAAAAATCAATGTGAAGCAGCCCGCCTCC 336
Qy   214 TGCCTCCGCTCACTCGCTGGTGTTCATCTTGTTTGTGGGCAACATGCTGGTCGTCTGG 273
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Db   337 TGCCTCCGCTCACTCACTGGTGTTCATCTTGTTTGTGGGCAACATGCTGGTCATCC 396
Qy   274 TCATCTTAATAAACTGCAAAAGCTGAAGTCGAAGTGCTTGACATTACCTGCTCAACCTGG 333
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Db   397 TCATCCTGATAAACTGCAAAAGCTGAAGCATGACATCTACCTGCTCAACCTGG 456
Qy   334 CCATCTCTGATCTGCTTTTCTATTACTCTCCATTGTGGGCTCACTGTGCTGCAAATG 393
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Db   457 CCATCTCTGACCTGTTTTTCCCTTCTTACTGTCCCCTTTCTGGGCCTCACTATGCTGCCCCC 516
Qy   394 AGTGGGTCTTTGGAATGCAAATGTGCAAATTATTCACAGGGCTGTATCACCGGTTATT 453
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Db   517 AGTGGGACTTTGGAAATACAATCGTCAACTCTTGACAGGCTCATTTTATAGGCTTCT 576
Qy   454 TTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATTGTCCATG 513
         ||  ||||||  |||| || |||| |||||||||||||||||||||||||||||||
Db   577 TCTCTGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTGTCGTCCATG 636
Qy   514 CTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACCT 573
         |||||||||| ||||||||| |||| |||||| ||| |||||||| |||||||| |||
Db   637 CTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTT 696
Qy   574 GGTGGTGGCTGTGTTGCTTCTTGTGTCCAGGAATCATCTTTACTAAAATGCCAGAAAGAAG 633
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Db   697 GGGTGGTGGCTGTGTTTGCGTCTCTCCCAGGAATCATCTTTACCAGATCTCAAAAGAGAAG 756
Qy   634 ATTCTGTTTATGTCTGTGGCCCTTATTTTCCA------CGAGGATGGAATAATT 681
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Db   757 GTCTTCATTACACCTGCAGCTCATTTTCATTTTCCATACAGTCCAGTATCAATTCTGGAAGAATT 816
Qy   682 TCCACACAATAATGAGGAACATTTGGGGCTGCTCCTGCCGCTGTCTCATCATGTGTCATCT 741
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Db   817 TCCAGACATTAAAGATAGTCATCTGGGGCTGCTCCTGCCGCTTGTCTGTCATCATGTCATCT 876
Qy   742 GCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTGTCGAAACGAGAAGAAGAGGCATAGGG 801
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Db   877 GCTACTCGGGAATCCTTAAAAACTCTGCTCTGCTGTCTCGGTGTCTCGAAATGAGAAGAAGAGGCACAGGG 936
Qy   802 CAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTGGACTCCCTATACA 861
         |  ||| || |||||| |||||||| | ||| ||| ||| |||||||||| | |||
Db   937 CTGTGAGGCTTATCTTCACCATCATGATTTTATTTTCTCTTCGGGCTCCCTACACAACA 996
Qy   862 TTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCA 921
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Db   997 TTGTCCTTCTCCTGAACACCTTCCAGGAATTCTTTGGCCTGCCTGAATAATTGCAGTAGCCTCTA 1056
Qy   922 GTCAACTGGACCAAGCCAGCCAGGCAGGTGACACGAGTCTTGGATGACTCACTGCTGCATCA 981
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Db  1057 ACAGGTTGGACCAAGCTATGCAGGTGACAGAGACTCTTGGGATGACCGCCACTGCTGCATCA 1116
Qy   982 ATCCCATCATCCTATGCCTTCGTTGGGGGAGGAGTTCAGAAGGTATCTCGTTGTTCTTCC 1041
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Db  1117 ACCCCATCATCTATGCCTTTGTCGCGGAGGAGTTCAGGAACAGTTTTCTTCGTTCTTTCC 1176
Qy  1042 GAAAGCACATCACCCAAGCGCTTCTGCCAAACAATGTCCAGTTTTCTACAGGAGACAGTGG 1101
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Db  1177 AAAAGCACATTGCCAAACGCTTGTGTTTCTATTTTCCAGCCAAGAGGCTTCCCG 1236
Qy  1102 ATGGAGTGACTTCAACAAACCGCCTTCCACTGGGAGTCAGCAGGAGTCGGCTGGTTTAT 1161
         ||| || ||  |||||  || ||| |||||||||||||| ||| ||  |||| ||||
Db  1237 AGCGAGCAAGCTCAGTTTACACCCGATCCACTGGGAGCAGGAAATATCGTGGGCTTGT 1296
Qy  1162 AAAACGAGGAGCAGTTGATTGT 1184
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Db  1297 GACACGGGACTCAAGTGGGCTGGT 1319
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RESULT 12

RESULT 13
US-10-106-623-1
; Sequence 1, Application US/10106623
Patent No. US2002015088A1
; GENERAL INFORMATION:
APPLICANT: Gray, Patrick W.
Schweickart, Vicky L.
Raport, Carol J.
TITLE OF INVENTION: Chemokine Receptor Materials and Methods
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/106,623
FILING DATE: 26-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/771,276
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: NO. US2002015088Aland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33670
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3383 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 55..1110
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: /= "88C polynucleotide and amino acid sequences"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-106-623-1

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Query Match       35.5%;    Score 703.4;    DB 12;    Length 3383;
Best Local Similarity    80.5%;    Pred. No. 5.6e-201;
Matches 840;    Conservative 0;    Mismatches 191;    Indels 12;    Gaps  1;

Qy    154 ATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAGCAAATTGGGGCCCAACTCC  213
          || |   ||| |||| ||||||| | |||  || || || ||||||  ||| |||||||
Db     92 ATTATTATACATCGGAGCCCTGCCAAAAAATCAATGTGAAGCAAATCGCAGCCGCCTCC  151

Qy    214 TGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTGTTGGGCAACATCTGGTCGTCC  273
          ||||||||||||||||| |||||||||||||||||||||||||||||||||||||| ||
Db    152 TGCCTCCGCTCTACTCACTGGTGTTCATCTTTGGTTTGTTGGGCAACATCTGGTCATCC  211

Qy    274 TCATCTTAATAAACTGCAAAAACTGAAGAGCTGCTGACATTTACCTGCTCAACCTGG    333
          ||||| | | ||||||||||| |||||||| || ||| ||| ||||||||| |||||
Db    212 TCATCCTGAAACTGCAAAAGGCTGAAGAGCATGACTGACATCACCTGCTCACCTGG    271

Qy    334 CCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGCCTCACTGTGTATCACATCGGTTATT  393
          |||||||||| ||| | |||| ||  ||| ||  |   ||| ||| |||| |  |||||||
Db    272 CCATCTCTGACCTGTTTTTCCTTCTACTGTCCCCTTCTCACTATGCTCGCCGCCC          331

Qy    394 AGTGGTCTTTGGGAATGCAATGTCAAATTATTCACACGGCTGTATCACATCGGTTATT  453
          ||||| ||||||| ||  |||||||| |  |||| |||| ||| |  |  || ||| |
Db    332 AGTGGGACTTTGGAAATACAATGTCAACTCTTGACAAGCTTCTTATTTTATAGGCTTCT  391

Qy    454 TTGGCGGAATCTTCTTCATCATCCTGACAATCGATAGATACCTGGCTATTGTCCATG    513
          | |||||||||||||||||||||||  ||||||||| || ||| |||  ||||||||
Db    392 TCTCTGGAATCTTCTTCATCATCCCTGCAATCGATAGATAGTGTCGTCGTCGTCCATG    451

Qy    514 CTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACCT  573
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    452 CTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTT  511

Qy    574 GGTTGGTGGCTGTGTTGCTTCTTCGTCTCCAGGAATCATCTTTACTAAATGCCAGAAAGAAG  633
          || | ||||||||||| ||  || | |||||||||||||||||||  |  || ||||||||
Db    512 GGGGTGGTGGCTGTGTTTGCGTCTCTCCCAGGAATCATCTTTACCAGAATCTCAAAAAGAAG  571

Qy    634 ATTCTGTTTATGTCTGTGCCCTTATTTTCCA---------CGAGGATGGAATAATT    681
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Db    572 GTCTTCATTTACACCTGCAGCTCTCATTTTCCATACAGTCAGTATCAATTCTGGAGAATT  631

Qy    682 TCCACACAATAATGAGGAACATTTGGGCTGGTCCTGCCGCTCCTCATCATGTCATCT    741
          |||| || | || |   |  || ||||| || ||||||||| || ||||| |||||
Db    632 TCCAGACATTAAAGATAGTCATCTTGGGGCGTCCTGGTCCTGCGTCCATGGTCATCT     691

Qy    742 GCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACAGAGAAGAGGCATAGGG    801
          |||||||||||||| |||| || || |||| ||| |||| ||| || ||| || ||||
Db    692 GCTACTCGGGAATCCTAAAAACCTGCTTCGGTGTCGAAATGAGAAGAAGAGGCACAGGG   751

Qy    802 CAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTTGCTTCTTCTTTGGACTCCCTATAACA  861
          | |||||  | |||||||||||||||| | |||| |||  | || || ||| || ||| |||||
Db    752 CTGTGAGGCGTTATCTTCACCATCATGATGTTTATTTTCCTTCTTCTGGCCTCCCTACAACA    811

Qy    862 TTGTCATTCCTGAACACCTTCCAGGAATTCTCGGCCTGAGTAACTGTGAAAGCACCA    921
          ||||| ||||||||||||||||||||||||| | |||||| || |||  | |  | |
Db    812 TTGTCCTTCCTGAACACCTTCCAGGAATTCTTTGGCCTGAATAATTGCAGTAGCTCTA    871

Qy    922 GTCAACTGGACCAAGCCACCACCGAGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCA  981
          | ||| |||||||||| | |  || |||||||||||||||||||||||| ||||||||||||
Db    872 ACAGGTTGGACCAAGCTATGCAGGTGACAGAGACTCTTGGGATGACGCACTGCTGCATCA    931

Qy    982 ATCCCATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTTCGGTGTTCTTCC  1041
          | ||||||||||||||||||||||| ||||||||||||| | | ||| | ||  |||||
Db    932 ACCCCATCATCTATGCCTTCGTTGCGGGAGAAGTTCAGAAACTACCTCTTAGTCTTCTTCC   991

Qy   1042 GAAAGCACATCACCAAGGCGTTCTGCCAAACAATGTCCAGTTTTCTACAGGGAGACAGTGG  1101
          |||||||||| |||||||| ||||||||||  |||| ||||||||  || | || |||  |
Db    992 AAAAGCACATTGCCAAAGGCTTCTGCCAAATCGTTCGTTTCTATTTTCCAGCAAGAGGCTCCCG  1051

Qy   1102 ATGGAGTGACTTCAACAAACACGCCTTCCACGGGAGCCAGGAAGTCTCGGCTGGTTTAT  1161
          | |||| | |  | || || |  ||| |||| |||||| |||| | |  |||| |||||
Db   1052 AGGGAGCAAGCCAGTTACCCGATCCACCGGGAGCCAGGAGAAATATCTGTGGGCGTTGT  1111

Qy   1162 AAAACGAGGAGCAGTTTGATTGT  1184
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Db   1112 GACACGGACTCAAGTGGGCTGGT  1134
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Query Match           35.5%;
Best Local Similarity 80.4%;                 Score 701.8;  DB 10;  Length 1225;
Matches  839;  Conservative   0;  Mismatches 192;          Pred. No. 8.4e-201;
                                             Indels  12;   Gaps  1;

Qy  154 ATTATGATTACGGTGCTCCGTGTCATAAATTGACGTGAAGCAAATTGGGCCCAACTCC   213
        |||| ||  ||| || |||||| ||||    |  ||||||||||  |||| ||||||
Db   64 ATTATTATACATCGGAGCCCTGCCAAAAAATCAATGTGAAGCAATCGGCAGCCCGCCCTCC 123

Qy  214 TGCCTCCGCTCACTCGCTGCTGTCATCTTTGGTTTTGTGGGCAACAATGCTCGTCGTCC   273
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Db  124 TGCCTCCGCTCACTCACTGGTTCATCTTTGGTTTTGTGGGCAACAATGCTCGTCATCC   183

Qy  274 TCATCTTAATAAACTGCAAAAGCTGAAGTGCTTGACTGACATTACCTGCTCAACCTGG   333
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Db  184 TCATCCAGATAAACTGCAAAAGGCTGAAGAGCCATGACATCGACATCACCTGCTCAACCTGG 243

Qy  334 CCATCTCGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCTGCAAATG   393
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Db  244 CCATCTCTGACCTGTTTTTCCTTCTTCTACTGTCCCCTTCTGGCTCACTGACTGCCGCCC   303

Qy  394 AGTGGGTCTTTGGGAATGCAAATGTGCAAATTATTCACAGGGCTGTATCACATCGGTTATT  453
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Db  304 AGTGGGACTTTGGAAATACAATGTGTCAACTCTTGACAGGGCCGCTCTATTTTATAGGCTTCT 363

Qy  454 TTGGCGGAATCTCTTCATCATCCTCGACAATCGATAGATACCTGCTATTGTCCATG      513
        |  | ||||||||||||||||||||||||||||||||| |||||| |  | | |||||
Db  364 TCTCTGGAATCTCTTCATCATCCTCGACAATCGATAGGTACCTGGCTGTCGTCGTCCATG   423

Qy  514 CTGTGTTTGCTTTAAAAGCCAGGACAGGTCACCTTTGGGGTGGTGACAAGTGTGATCACCT  573
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db  424 CTGTGTTTGCTTTAAAAGCCAGGACAGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTT  483

Qy  574 GGTTGGTGGCGTGTGTTGCGTCTCTCCCAGGAATCATCTTTACTAAATGCCAGAAAGAAG   633
        || ||||||||||||||||||||||||||||||||||||||   |  || ||| ||||||
Db  484 GGGTGGTGGCGTGTGTTGCGTCTCTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAG   543

Qy  634 ATTCTGTTTATGTCTGCTGGGCCCTTATTTCCA---------CGGGATGGAATAATT     681
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Db  544 GTCTTCATTACACCTGCAGCTCTCATTTTCCATACAGTCAGTATCAATTCTGGAAGAATT   603

Qy  682 TCCACACAATAATGAGGAACATTGGGGCTGGCTCCTGCCCGCTGGTCCTGTTGTCATGGTCATCT 741
        ||||  ||| || || ||||| ||| ||| |||||||| | | | | |||| | |||| |||
Db  604 TCCAGACATTAAAGATAGTCATCTTGGGGCTGGCTCCTGCCCGCTGGTCCTGTTGTCATGGTCATCT 663

Qy  742 GCTACTCGGGAATCCTGAAAACCGCTTCGGTGTCGAAACGAGAAGAGGCATAGGG       801
        |||||||||||||| |||||| | ||| ||||||| || ||||||| || ||||
Db  664 GCTACTCGGGAATCCTAAAAACTCGCTCGGTGTCGAAATGAGAAGAGGAGGCACAGGG     723

Qy  802 CAGTGAGAGTCATCTTCACCATCATGATTGTTACTTTCTTCTTGGGACTCCCTATAACA    861
        ||||||| | ||| |||||||||||| | |||  |||| | ||||| ||||| | | ||
Db  724 CTGTGAGGCTTATCTTCACCATCATGATTGTTATTTTCTTCTTGGGCTCCCTCCTACAACA   783

Qy  862 TTGTCATTCCTGAACACCTTCAGTGGGGGAACAATGTCCAGTTTTCTACAGGGAGACAGTGG 921
        ||||| ||||||||||||||| | |  ||| || ||  |||| |  | | ||| ||||||||
Db  784 TTGTCCTTCCTGAACACCTTCCAGAGGTGACAGTCGGAGGTTCAGAGTTCAGAAACTACCTCTA 843

Qy  922 GTCAACTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCA    981
        |||||||||||||||||| | |||||||||  | || |||||||| |||| |||||||||
Db  844 ACAGGTTGGACCAAGCCAAGCTATGCAGGTGACGACAGAGACTGCTGCTGCATCA       903

Qy  982 ATCCCATCATCTATGCCTTCGTTGGGGGAAGTTCAGAAGGTCATCCTCGGTTGTTCTTCC   1041
        | ||||||||||| || ||| | |||||| |||||| | ||||  |  |  ||| ||||
Db  904 ACCCCATCATCTATGCCTTTGTCGGGGGAGCAGGAGGAAGTTCAGAAACTACCACCTCTTAGTCTTCTTCC 963

Qy 1042 GAAAGCACAATCACCAAGCCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACACCA  1101
        ||||||| | | ||||||| | |||||||| | |||| |||||||| | |||| ||| |||
Db  964 AAAAGCACCATTGCCAAACGCCTTCTGCAAATGCTGTGTTCTATTTTCCAGCAAGAGAGGCTCCCG 1023

Qy 1102 ATGGAGTGACTTCAACAAACGCCTTCGGTGTTTAT                          1161
        | | ||  || | ||||| | || || |||| ||
Db 1024 AGCGAGCAAGCTCAGTTTACACCCGATCCACTGGGGAGCAGGAAATATCTGTGGGCTTGT  1083

Qy 1162 AAAACGAGGAGCAGTTTGATTGT                                      1184
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Db  512 GGGTGGTGGCGTGTGTTGCGTCTCTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAG   571
Qy  634 ATTCTGTTTATGTCTGCTGGGCCCTTATTTCCA---------CGGGATGGGAATAATT     681
Db  572 GTCTTCATTACACCTGCAGCTCTCATTTTCCATACAGTCAGTATCAATTCTGGAAGAATT   631
Qy  682 TCCACACAATAATGAGGAACATTGGGGCTGGCTCCTGCCCGCTGGTCCTGTTGTCATGGTCATCT 741
Db  632 TCCAGACATTAAAGATAGTCATCTTGGGGCTGGCTCCTGCCCGCTGGTCCTGTTGTCATGGTCATCT 691
Qy  742 GCTACTCGGGAATCCTGAAAACCGCTTCGGTGTCGAAACGAGAAGAGGCATAGGG       801
Db  692 GCTACTCGGGAATCCTAAAAACTCGCTCGGTGTCGAAATGAGAAGAGGAGGCACAGGG     751
Qy  802 CAGTGAGAGTCATCTTCACCATCATGATTGTTACTTTCTTCTTGGGACTCCCTATAACA    861
Db  752 CTGTGAGGCTTATCTTCACCATCATGATTGTTATTTTCTTCTTGGGCTCCCTCCTACAACA   811
Qy  862 TTGTCATTCCTGAACACCTTCAGTGGGGGAACAATGTCCAGTTTTCTACAGGGAGACAGTGG 921
Db  812 TTGTCCTTCCTGAACACCTTCCAGAGGTGACAGTCGGAGGTTCAGAGTTCAGAAACTACCTCTA 871
Qy  922 GTCAACTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCA    981
Db  872 ACAGGTTGGACCAAGCCAAGCTATGCAGGTGACGACAGAGACTGCTGCTGCATCA       931
Qy  982 ATCCCATCATCTATGCCTTCGTTGGGGGAAGTTCAGAAGGTCATCCTCGGTTGTTCTTCC   1041
Db  932 ACCCCATCATCTATGCCTTTGTCGGGGGAGCAGGAGGAAGTTCAGAAACTACCACCTCTTAGTCTTCTTCC 991
Qy 1042 GAAAGCACAATCACCAAGCCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACACCA  1101
Db  992 AAAAGCACCATTGCCAAACGCCTTCTGCAAATGCTGTGTTCTATTTTCCAGCAAGAGAGGCTCCCG 1051
Qy 1102 ATGGAGTGACTTCAACAAACGCCTTCGGTGTTTAT                          1161
Db 1052 AGCGAGCAAGCTCAGTTTACACCCGATCCACTGGGGAGCAGGAAATATCTGTGGGCTTGT  1111
Qy 1162 AAAACGAGGAGCAGTTTGATTGT                                      1184
Db 1112 GACACGGACTCAAGTGGGCTGGT                                      1134
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RESULT 14
US-09-813-653-16
; Sequence 16, Application US/09813653
; Patent No. US2002006477OA1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehir, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 1225
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27)..(1085)
US-09-813-653-16

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RESULT 15
US-10-232-686-1

; Sequence 1, Application US/10232686
; Publication No. US20030023044A1
; GENERAL INFORMATION:
;   APPLICANT: Li, Yi
;   APPLICANT: Ruben, Steven M.
;   TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNR10
;   FILE REFERENCE: 1488.115000N
;   CURRENT APPLICATION NUMBER: US/10/232,686
;   CURRENT FILING DATE:  2002-09-03
;   PRIOR APPLICATION NUMBER: 09/339,912
;   PRIOR FILING DATE: 1999-06-25
;   PRIOR APPLICATION NUMBER: 09/195,662
;   PRIOR FILING DATE: 1998-11-18
;   PRIOR APPLICATION NUMBER: 08/466,343
;   PRIOR FILING DATE: 1995-06-06
;   NUMBER OF SEQ ID NOS: 9
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 1414
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (259)..(1314)
US-10-232-686-1

Query Match   35.5%;  Score 701.8;  DB 9;  Length 1414;
Best Local Similarity   80.4%;  Pred. No. 9.3e-201;
Matches  839;  Conservative   0;  Mismatches  192;  Indels  12;  Gaps  1;

Qy    154 ATTATGATTACGGTGCTCCCTGTCATAAATTGACGTGAAGCAAATTGGGGCCCAACTCC 213
              |||| ||| |  ||||||| ||   | ||||||||||||| | |||| ||||
Db    296 ATTATTATACATCGGAGCCCTGCCAAAAAATCAATGTGAAGCAAATCGCAGCCCCGCCTCC 355

Qy    214 TGCCTCCGCTCACTCGCCTGGTGTTCATCTTTGGTTTGTGGGCAACATGCTGGTCGTCC 273
              |||||||||||| ||||||||| |||||||||||| |||||||||||||||||||||
Db    356 TGCCCCCGCCTCACTCACTCGGTGTTCATCTTTGGTTTGTGGGCAACATGCTGGTCATCC 415

Qy    274 TCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTCAACCTGG 333
              |||| || | |||| ||||||||  ||||| |||| || |||||| |||||||||||||
Db    416 TCATCCTGATAAACTGCAAAAGGCTGAAGAGCATGACATCTGCTCAACCTGG 475

Qy    334 CCATCTCTGATCTGCTTTTTCTTATTACTCCTCCCATTGTGGCTCACTCTGCTGCAAATG 393
              |||||||||||| |||| ||| ||| |||| ||| || ||||||||| |||| |||||
Db    476 CCATCTCTGACCTGTTTTTCCCTTCTACTGCCCCTCTGGGCTCACTATGCTGCCGCCC 535

Qy    394 AGTGGGCTCTTGGGAATGCAATGTCGCAAATTATTCACAGGGCTGTATCACATCGGTTATT 453
              |||||||| |||||||||  || |  || |||  || ||||| |||| ||||| ||||
Db    536 AGTGGGACTTTGGAAATACAATGTGTCAACTCTTGGGGTTGTTTGTGGCCAACATGCTGGTCATCC 595

Qy    454 TTGGCCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATTGTCCATG 513
              |||||||||||||  |||||||| |||||||||| ||||| |  |||||| ||| ||||||
Db    596 TCTCTGGAATCTTCTTCATCATCCTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATG 655

Qy    514 CTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGCTCACTTGCTATCACACCT 573
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db    656 GGGTGGTGGCTGGTGTTTGCGGTCGTCCATGCTATCTTACCAGATCTCAAAAGAAG 715

Qy    574 GGTTGGTGGCTGGTGTTTGCTTGTTCTCGTCCCAGGAATCATCTTTACTAAATGCCAGAAGAAG 633
              |||||||||||||||||||  || || |||| ||||| |||||||| ||| |||||||||||
Db    716 GGGTGGTGGCTGGTGTTTGCGGTCTCCGGAATCATCTTTACCAGATCTCAAAAGAAG 775

Qy    634 ATTCTGTTTATGTCTGGCCCTTATTTCCA-------CGAGGATGGAATAATT 681
              | |  |||  |||||| |||||| |||        | | || |||| || |
Db    776 GTCTTCATTACCACCTGCAGCTCCATTTTCCATACAGTCAGTATCAATTCTGGAAGAATT 835

Qy    682 TCCACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATCT 741
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